

WHAT IS CLAIMED IS:

1. A computer readable medium having stored thereon a sequence selected from the group consisting of a nucleic acid code of SEQID NOS. 1,2, 5,9,  
5 13,25,27,29, 31,33, 37,41,45, 57, 59, 61, 63, 65, 67,71, 75, 79, 3, 7, 11, 15, 17, 19,21,23, 35, 39, 43,47,49, 51, 53, 55, 69, 73 and 77 and a polypeptide code of SEQ ID NOS. 6, 10, 14, 26,28, 30, 32, 34, 38, 42, 46, 58, 60, 62, 64, 66, 68, 72, 76, 80, 4, 8, 12, 16, 18, 20, 22, 24,36,40,44,48, 50, 52, 54, 56, 70,74, and 78.
- 10 2. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a sequence selected from the group consisting of a nucleic acid code of SEQID NOS. 1,2, 5, 9, 13, 25, 27, 29, 31, 33, 37, 41, 45, 57, 59, 61, 63, 65, 67,71, 75, 79, 3, 7, 11, 15, 17, 19,21, 23, 35, 39,43,47,49, 51, 53, 55, 69, 73 and 77 and a polypeptide code of SEQ ID NOS. 6, 10, 14,26,28,30, 32, 34, 38, 42,46, 58, 60, 62, 64, 66, 68, 72, 76, 80, 4, 8, 12, 16, 18, 20, 22, 24, 36, 40, 44, 48, 50, 52, 54, 56, 70, 74, and 78.
- 15 3. The computer system of Claim 2 further comprising a sequence comparer and a data storage device having reference sequences stored thereon.
4. The computer system of Claim 3 wherein said sequence comparer comprises a computer program which indicates polymorphisms.
- 20 5. The computer system of Claim 2 further comprising an identifier which identifies features in said sequence.
6. A method for comparing a first sequence to a reference sequence wherein said first sequence is selected from the group consisting of a nucleic acid code of SEQID NOS. 1,2, 5,9, 13,25,27,29, 31,33, 37,41,45, 57, 59, 61,63,65,67,71,75, 79, 3,7, 11, 15, 17, 19, 21, 23, 35, 39, 43, 47, 49, 51, 53, 55, 69, 73 and 77 and a polypeptide code of SEQ ID NOS. 6, 10, 14,26,28, 30, 32, 34, 38, 42,46, 58, 60, 62, 64, 66, 68, 72, 76, 80, 4, 8, 12, 16, 18, 20, 22, 24, 36, 40, 44, 48, 50, 52, 54, 56, 70, 74, and 78 comprising the steps of  
25 reading said first sequence and said reference sequence through use of a computer program which compares sequences; and  
30

determining differences between said first sequence and said reference sequence with said computer program.

7. The method of Claim 6, wherein said step of determining differences between the first sequence and the reference sequence comprises identifying polymorphisms.

8. A method for identifying a feature in a sequence selected from the group consisting of a nucleic acid code of SEQID NOS. 1,2, 5, 9, 13, 25, 27, 29, 31, 33, 37, 41, 45, 57, 59, 61, 63, 65, 67, 71, 75, 79, 3, 7, 11, 15, 17, 19, 21, 23, 35, 39, 43, 47,49, 51, 53,55,69,73 and 77 and a polypeptide code of SEQ ID NOS. 6, 10, 14,26,28,30,32, 34, 38, 42, 46, 58, 60, 62, 64, 66, 68, 72, 76, 80, 4, 8, 12, 16, 18, 20, 22, 24, 36, 40, 44, 48, 50, 52, 54, 56, 70, 74, and 78 comprising the steps of:

reading said sequence through the use of a computer program which identifies features in sequences; and

identifying features in said sequence with said computer program.